



Revised sequence listing2  
SEQUENCE LISTING

<110> Stratagene  
<120> HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR  
<130> 25436/2155  
<140> 10/079,241  
<141> 2002-02-20  
<160> 23  
<170> PatentIn version 3.1  
<210> 1  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Conserved domain  
<220>  
<221> MISC\_FEATURE  
<222> (2)..(3)  
<223> Conserved domain, X at position 2 or 3 is any amino acid.

<400> 1

Asp Xaa Xaa Ser Leu Tyr Pro  
1 5

<210> 2  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Conserved domain  
<220>  
<221> MISC\_FEATURE  
<222> (2)..(7)  
<223> Conserved domain, X at position 2, 3, 4, or 7 is any amino acid.

<400> 2

Lys Xaa Xaa Xaa Asn Ser Xaa Tyr Gly  
1 5

<210> 3  
<211> 5  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Conserved domain

## Revised sequence listing2

<220>  
 <221> misc\_feature  
 <222> (2)..(3)  
 <223> Conserved domain, X at position 2 or 3 is any amino acid.

<400> 3

Thr Xaa Xaa Gly Arg  
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<210> 4  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Conserved domain

<220>  
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 <222> (2)..(2)  
 <223> Conserved domain, X at position 2 is any amino acid.

<400> 4

Tyr Xaa Asp Thr Asp Ser  
 1 5

<210> 5  
 <211> 3  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Conserved domain

<220>  
 <221> misc\_feature  
 <222> (2)..(2)  
 <223> Conserved domain, X at position 2 is any amino acid.

<400> 5

Lys Xaa Tyr  
 1

<210> 6  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Conserved domain

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)

# Revised sequence listing2

<223> Conserved domain, X at position 2 is any amino acid.

<400> 6

Tyr Xaa Gly Gly  
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<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved domain

<220>

<221> MISC\_FEATURE

<222> (1)..(6)

<223> Conserved domain

<400> 7

Ser Tyr Thr Gly Gly Phe  
1 5

<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<220>

<221> misc\_feature

<222> (1)..(23)

<223> Synthetic primer

<400> 8

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23

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<220>

<221> misc\_feature

<222> (1)..(23)

<223> Synthetic primer

<400> 9

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23

# Revised sequence listing2

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 <212> PRT  
 <213> Thermococcus sp. JDF-3

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile  
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Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg  
 20 25 30

Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile  
 35 40 45

Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys  
 50 55 60

Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val  
 65 70 75 80

Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile  
 85 90 95

Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr  
 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro  
 115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr  
 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile  
 145 150 155 160

Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile  
 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys  
 180 185 190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr  
 195 200 205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu  
 210 215 220

# Revised sequence listing2

Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys  
 225 230 235 240  
 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val  
 245 250 255  
 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr  
 260 265 270  
 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu  
 275 280 285  
 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly  
 290 295 300  
 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr  
 305 310 315 320  
 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu  
 325 330 335  
 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu  
 340 345 350  
 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala  
 355 360 365  
 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr  
 370 375 380  
 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile  
 385 390 395 400  
 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His  
 405 410 415  
 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp  
 420 425 430  
 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe  
 435 440 445  
 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys  
 450 455 460

Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp  
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465		470		475		480
Tyr	Arg	Gln	Arg	Ala 485	Ile	Lys
Ile	Leu	Ala 490	Asn	Ser	Tyr	Tyr
Gly 495	Tyr					
Tyr	Gly	Tyr	Ala 500	Arg	Ala	Arg
Trp	Tyr 505	Cys	Arg	Glu	Cys	Ala
Glu	Ser					
Val	Thr	Ala 515	Trp	Gly	Arg	Glu
Tyr 520	Ile	Glu	Met	Val	Ile 525	Arg
Glu	Leu					
Glu	Glu	Lys	Phe	Gly	Phe	Lys
Val 530	Leu	Tyr	Ala	Asp 540	Thr	Asp
Gly	Leu					
His	Ala	Thr	Ile	Pro	Gly 550	Ala
Asp	Ala	Glu	Thr 555	Val	Lys	Lys
Lys	Lys	Lys	Ala 560			
Met	Glu	Phe	Leu	Asn 565	Tyr	Ile
Asn	Pro	Lys 570	Leu	Pro	Gly	Leu
Leu 575	Glu					
Leu	Glu	Tyr	Glu 580	Gly	Phe	Tyr
Val	Arg 585	Gly	Phe	Phe	Val	Thr
Lys	Lys					
Lys	Tyr	Ala 595	Val	Ile	Asp	Glu
Glu 600	Gly	Lys	Ile	Thr	Thr 605	Arg
Gly	Leu					
Glu	Ile	Val	Arg	Arg	Asp	Trp
Ser	Glu	Ile	Ala	Lys 620	Glu	Thr
Gln	Ala					
Arg	Val	Leu	Glu	Ala	Ile 630	Leu
Arg	His	Gly	Asp 635	Val	Glu	Glu
Ala	Val 640					
Arg	Ile	Val	Arg	Glu 645	Val	Thr
Glu	Lys	Leu 650	Ser	Lys	Tyr	Glu
Val 655	Pro					
Pro	Glu	Lys	Leu 660	Val	Ile	His
Glu	Gln 665	Ile	Thr	Arg	Glu	Leu
Lys	Asp					
Tyr	Lys	Ala 675	Thr	Gly	Pro	His
Val 680	Ala	Ile	Ala	Lys	Arg 685	Leu
Ala	Ala					
Arg	Gly	Val	Lys	Ile	Arg	Pro
Gly 690	Thr	Val	Ile	Ser 700	Tyr	Ile
Val	Leu					
Lys	Gly	Ser	Gly	Arg	Ile 710	Gly
Asp	Arg	Ala	Ile 715	Pro	Phe	Asp
Glu	Phe 720					

# Revised sequence listing2

Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln  
725 730 735

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys  
740 745 750

Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp  
755 760 765

Leu Lys Pro Lys Gly Lys Lys Lys  
770 775

<210> 11  
<211> 2331  
<212> DNA  
<213> Thermococcus sp. JDF-3

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ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc 180  
agggtcgtta aggttaagcg cgcgagagaag gtgaagaaaa agttcctcgg caggtctgtg 240  
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agggggggct acgccggtg ctacgtcaag gagccggagc ggggactgtg ggacaatatc 1200  
gtgtatctag actttcgtag tctctaccct tcaatcataa tcaccacaa cgtctcgcca 1260

# Revised sequence listing2

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<210> 12  
 <211> 6  
 <212> PRT  
 <213> *Pyrococcus furiosus*

<400> 12

Ser Tyr Thr Gly Gly Phe  
 1 5

<210> 13  
 <211> 6  
 <212> PRT  
 <213> *Thermococcus* sp.

<400> 13

Ser Tyr Ala Gly Gly Tyr  
 1 5

<210> 14  
 <211> 6  
 <212> PRT

# Revised sequence listing2

<213> Pyrococcus sp.

<400> 14

Ser Tyr Glu Gly Gly Tyr  
1 5

<210> 15

<211> 6

<212> PRT

<213> Thermococcus litoralis

<400> 15

Thr Tyr Leu Gly Gly Tyr  
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<210> 16

<211> 6

<212> PRT

<213> Pyrococcus sp.

<400> 16

Ser Tyr Ala Gly Gly Tyr  
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<210> 17

<211> 8

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<213> Artificial

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<221> MISC\_FEATURE

<222> (2)..(3)

<223> X = any amino acid

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<210> 18

<211> 7

<212> PRT

<213> Pyrococcus furiosus

<400> 18

Asp Phe Arg Ala Leu Tyr Pro  
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<210> 19

<211> 7

# Revised sequence listing2

<212> PRT  
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<400> 19

Asp Phe Arg Ser Leu Tyr Pro  
1 5

<210> 20  
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<220>  
<223> Polymerase domain consensus sequence

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<222> (2)..(2)  
<223> X = any amino acid

<400> 20

Tyr Xaa Asp Thr Asp Ser  
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<210> 21  
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<213> Pyrococcus furiosus

<400> 21

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<210> 22  
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<212> PRT  
<213> Thermococcus sp.

<400> 22

Tyr Ala Asp Thr Asp Gly  
1 5

<210> 23  
<211> 6  
<212> PRT  
<213> Pyrococcus sp.

<400> 23

Tyr Ser Asp Thr Asp Gly  
1 5